

00 71 2093

# SEQUENCE LISTING

SEQ ID NO: 1 is mouse TECK nucleotide sequence.  
SEQ ID NO: 2 is mouse TECK amino acid sequence.  
SEQ ID NO: 3 is human TECK nucleotide sequence.  
SEQ ID NO: 4 is human TECK amino acid sequence.  
SEQ ID NO: 5 is human MIP-3 $\alpha$  nucleotide sequence.  
SEQ ID NO: 6 is human MIP-3 $\alpha$  amino acid sequence.  
SEQ ID NO: 7 is human MIP-3 $\beta$  nucleotide sequence.  
SEQ ID NO: 8 is human MIP-3 $\beta$  amino acid sequence.  
SEQ ID NO: 9 is human DC CR nucleotide sequence.  
SEQ ID NO: 10 is human DC CR amino acid sequence.  
SEQ ID NO: 11 is human M/DC CR nucleotide sequence.  
SEQ ID NO: 12 is human M/DC CR amino acid sequence.  
SEQ ID NO: 13 is human CCKR1 amino acid sequence.  
SEQ ID NO: 14 is human CCKR2 amino acid sequence.  
SEQ ID NO: 15 is human CCKR3 amino acid sequence.  
SEQ ID NO: 16 is human CCKR4 amino acid sequence.  
SEQ ID NO: 17 is HPRT sense primer.  
SEQ ID NO: 18 is HPRT antisense primer.  
SEQ ID NO: 19 is FLAG epitope tag sequence.  
SEQ ID NO: 20 is TECK sense primer  
SEQ ID NO: 21 is TECK antisense primer  
SEQ ID NO: 22 is exon 1-specific CRAM primer  
SEQ ID NO: 23 is exon 2-specific CRAM primer  
SEQ ID NO: 24 is exon 3-specific CRAM primer  
SEQ ID NO: 25 is CRAM primer  
SEQ ID NO: 26 is CRAM primer

<110> Wang, Wei

Gish, Kurt C.

Schall, Thomas J.

Vicari, Alain P.

Zlotnik, Albert

<120> Antibodies that bind chemokine TECK

<130> DX0589K1B US

<140> US 10/039,659

<141> 2002-01-03

<150> US 08/887,977

<151> 1997-07-03

<150> US 60/021,664

<151> 1996-07-05

<150> US 60/028,329

<151> 1996-10-11

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<151> 1997-06-04

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<170> PatentIn version 3.1

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Gln Gly Ala Phe Glu Asp Cys Cys Leu Gly Tyr Gln His Arg Ile Lys  
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90 95 100

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Gln Thr Glu Arg Lys Lys Ser Asn His Met Lys Ser Lys Val Glu Asn  
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Tyr His Gln Gln Glu Val Ser Gly Ser Cys Asn Leu Arg Ala Val Arg  
50 55 60

Phe Tyr Phe Arg Gln Lys Val Val Cys Gly Asn Pro Glu Asp Met Asn  
65 70 75 80

Val Lys Arg Ala Ile Arg Ile Leu Thr Ala Arg Lys Arg Leu Val His  
85 90 95

Trp Lys Ser Ala Ser Asp Ser Gln Thr Glu Arg Lys Lys Ser Asn His  
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Tyr His Tyr Pro Ile Gly Trp Ala Val Leu Arg Arg Ala Trp Thr Tyr  
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Arg Ile Gln Glu Val Ser Gly Ser Cys Asn Leu Pro Ala Ala Ile Phe  
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Tyr Leu Pro Lys Arg His Arg Lys Val Cys Gly Asn Pro Lys Ser Arg  
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Glu Val Gln Arg Ala Met Lys Leu Leu Asp Ala Arg Asn Lys Val Phe  
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gca aag ctc cac cac aac atg cag acc ttc caa gca ggc cct cat gct 455

Ala Lys Leu His His Asn Met Gln Thr Phe Gln Ala Gly Pro His Ala  
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 Val Lys Lys Leu Ser Ser Gly Asn Ser Lys Leu Ser Ser Ser Lys Phe  
 95 100 105

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 Ser Asn Pro Ile Ser Ser Ser Lys Arg Asn Val Ser Leu Leu Ile Ser  
 110 115 120

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 Ala Asn Ser Gly Leu  
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ccggatcttt ctccgataaa accgtcgccc tacagacca gctgtcccca cgcctctgtc 666

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Tyr Arg Ile Gln Glu Val Ser Gly Ser Cys Asn Leu Pro Ala Ala Ile  
 30 35 40

Phe Tyr Leu Pro Lys Arg His Arg Lys Val Cys Gly Asn Pro Lys Ser  
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Arg Glu Val Gln Arg Ala Met Lys Leu Leu Asp Ala Arg Asn Lys Val  
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Phe Ala Lys Leu His His Asn Met Gln Thr Phe Gln Ala Gly Pro His  
       75                                  80                                  85

Ala Val Lys Lys Leu Ser Ser Gly Asn Ser Lys Leu Ser Ser Ser Lys  
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gtt ctc tgg act tcc cca gcc cca act ctg agt ggc acc aat gat gct 219  
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gaa gac tgc tgc ctg tct gtg acc cag aaa ccc atc cct ggg tac atc 267  
Glu Asp Cys Cys Leu Ser Val Thr Gln Lys Pro Ile Pro Gly Tyr Ile  
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gct gta gtg ttc acc aca ctg agg ggc cgc cag ctc tgt gca ccc cca 363  
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gac cag ccc tgg gta gaa cgc atc atc cag aga ctg cag agg acc tca 411  
Asp Gln Pro Trp Val Glu Arg Ile Ile Gln Arg Leu Gln Arg Thr Ser  
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Val Thr Gln Lys Pro Ile Pro Gly Tyr Ile Val Arg Asn Phe His Tyr  
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Leu Leu Ile Lys Asp Gly Cys Arg Val Pro Ala Val Val Phe Thr Thr  
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Gly Ser Ser Pro Gly Tyr Leu Tyr Arg Ile Ala Tyr Ser Leu Ile Cys  
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Val Leu Gly Leu Leu Gly Asn Ile Leu Val Val Ile Thr Phe Ala Phe  
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tat aag aag gcc agg tct atg aca gac gtc tat ctc ttg aac atg gcc 240  
Tyr Lys Lys Ala Arg Ser Met Thr Asp Val Tyr Leu Leu Asn Met Ala  
65 70 75 80

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Gly	Lys	Met	Asn	Arg	Ser	Cys	Gln	Ser	Glu	Lys	Leu	Ile	Gly	Tyr	Thr		
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aaa	act	gtc	aca	gaa	gtc	ctg	gct	ttc	ctg	cac	tgc	tgc	ctg	aac	cct	912	
Lys	Thr	Val	Thr	Glu	Val	Leu	Ala	Phe	Leu	His	Cys	Cys	Leu	Asn	Pro		
	290					295				300							
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Val Leu Tyr Ala Phe Ile Gly Gln Lys Phe Arg Asn Tyr Phe Leu Lys  
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 325 330 335

ttc tcc tgt gcc ggg agg tac tca gaa aac att tct cgg cag acc agt 1056  
 Phe Ser Cys Ala Gly Arg Tyr Ser Glu Asn Ile Ser Arg Gln Thr Ser  
 340 345 350

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Gly Ser Ser Pro Gly Tyr Leu Tyr Arg Ile Ala Tyr Ser Leu Ile Cys  
 35 40 45

Val Leu Gly Leu Leu Gly Asn Ile Leu Val Val Ile Thr Phe Ala Phe  
 50 55 60

Tyr Lys Lys Ala Arg Ser Met Thr Asp Val Tyr Leu Leu Asn Met Ala  
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Ile Ala Asp Ile Leu Phe Val Leu Thr Leu Pro Phe Trp Ala Val Ser  
 85 90 95

His Ala Thr Gly Ala Trp Val Phe Ser Asn Ala Thr Cys Lys Leu Leu  
 100 105 110

Lys Gly Ile Tyr Ala Ile Asn Phe Asn Cys Gly Met Leu Leu Leu Thr  
 115 120 125

Cys Ile Ser Met Asp Arg Tyr Ile Ala Ile Val Gln Ala Thr Lys Ser  
 130 135 140

Phe Arg Leu Arg Ser Arg Thr Leu Pro Arg Ser Lys Ile Ile Cys Leu  
 145 150 155 160

Val Val Trp Gly Leu Ser Val Ile Ile Ser Ser Ser Thr Phe Val Phe  
 165 170 175

Asn Gln Lys Tyr Asn Thr Gln Gly Ser Asp Val Cys Glu Pro Lys Tyr  
 180 185 190

Gln Thr Val Ser Glu Pro Ile Arg Trp Lys Leu Leu Met Leu Gly Leu  
 195 200 205

Glu Leu Leu Phe Gly Phe Phe Ile Pro Leu Met Phe Met Ile Phe Cys  
 210 215 220

Tyr Thr Phe Ile Val Lys Thr Leu Val Gln Ala Gln Asn Ser Lys Arg  
 225 230 235 240

His Lys Ala Ile Arg Val Ile Ile Ala Val Val Leu Val Phe Leu Ala  
 245 250 255

Cys Gln Ile Pro His Asn Met Val Leu Leu Val Thr Ala Ala Asn Leu  
 260 265 270

Gly Lys Met Asn Arg Ser Cys Gln Ser Glu Lys Leu Ile Gly Tyr Thr  
 275 280 285

Lys Thr Val Thr Glu Val Leu Ala Phe Leu His Cys Cys Leu Asn Pro  
 290 295 300

Val Leu Tyr Ala Phe Ile Gly Gln Lys Phe Arg Asn Tyr Phe Leu Lys  
 305 310 315 320

Ile Leu Lys Asp Leu Trp Cys Val Arg Arg Lys Tyr Lys Ser Ser Gly  
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gaggaagctg cttcgggggg tgagcaaact ttttaaaatg cagaaatt atg atc tac 57  
Met Ile Tyr  
1

acc cgt ttc tta aaa ggc agt ctg aag atg gcc aat tac acg ctg gca 105  
Thr Arg Phe Leu Lys Gly Ser Leu Lys Met Ala Asn Tyr Thr Leu Ala  
5 10 15

cca gag gat gaa tat gat gtc ctc ata gaa ggt gaa ctg gag agc gat 153  
Pro Glu Asp Glu Tyr Asp Val Leu Ile Glu Gly Glu Leu Glu Ser Asp  
20 25 30 35

gag gca gag caa tgt gac aag tat gac gcc cag gca ctc tca gcc cag 201  
Glu Ala Glu Gln Cys Asp Lys Tyr Asp Ala Gln Ala Leu Ser Ala Gln  
40 45 50

ctg gtg cca tca ctc tgc tct gct gtg ttt gtg atc ggt gtc ctg gac 249  
Leu Val Pro Ser Leu Cys Ser Ala Val Phe Val Ile Gly Val Leu Asp  
55 60 65

aat ctc ctg gtt gtg ctt atc ctg gta aaa tat aaa gga ctc aaa cgc 297  
Asn Leu Leu Val Val Leu Ile Leu Val Lys Tyr Lys Gly Leu Lys Arg  
70 75 80

gtg gaa aat atc tat ctt cta aac ttg gca gtt tct aac ttg tgt ttc 345

Val	Glu	Asn	Ile	Tyr	Leu	Leu	Asn	Leu	Ala	Val	Ser	Asn	Leu	Cys	Phe		
85						90					95						
ttg	ctt	acc	ctg	ccc	ttc	tgg	gct	cat	gct	ggg	ggc	gat	ccc	atg	tgt	393	
Leu	Leu	Thr	Leu	Pro	Phe	Trp	Ala	His	Ala	Gly	Gly	Asp	Pro	Met	Cys		
100					105					110					115		
aaa	att	ctc	att	gga	ctg	tac	ttc	gtg	ggc	ctg	tac	agt	gag	aca	ttt	441	
Lys	Ile	Leu	Ile	Gly	Leu	Tyr	Phe	Val	Gly	Leu	Tyr	Ser	Glu	Thr	Phe		
				120					125					130			
ttc	aat	tgc	ctt	ctg	act	gtg	caa	agg	tac	cta	gtg	ttt	ttg	cac	aag	489	
Phe	Asn	Cys	Leu	Leu	Thr	Val	Gln	Arg	Tyr	Leu	Val	Phe	Leu	His	Lys		
			135					140					145				
ggc	aac	ttt	ttc	tca	gcc	agg	agg	agg	gtg	ccc	tgt	ggc	atc	att	aca	537	
Gly	Asn	Phe	Phe	Ser	Ala	Arg	Arg	Arg	Val	Pro	Cys	Gly	Ile	Ile	Thr		
		150					155					160					
agt	gtc	ctg	gca	tgg	gta	aca	gcc	att	ctg	gcc	act	ttg	cct	gaa	ttc	585	
Ser	Val	Leu	Ala	Trp	Val	Thr	Ala	Ile	Leu	Ala	Thr	Leu	Pro	Glu	Phe		
	165					170					175						
gtg	gtt	tat	aaa	cct	cag	atg	gaa	gac	cag	aaa	tac	aag	tgt	gca	ttt	633	
Val	Val	Tyr	Lys	Pro	Gln	Met	Glu	Asp	Gln	Lys	Tyr	Lys	Cys	Ala	Phe		
180					185					190					195		
agc	aga	act	ccc	ttc	ctg	cca	gct	gat	gag	aca	ttc	tgg	aag	cat	ttt	681	
Ser	Arg	Thr	Pro	Phe	Leu	Pro	Ala	Asp	Glu	Thr	Phe	Trp	Lys	His	Phe		
			200						205					210			
ctg	act	tta	aaa	atg	aac	att	tcg	gtt	ctt	gtc	ctc	ccc	cta	ttt	att	729	
Leu	Thr	Leu	Lys	Met	Asn	Ile	Ser	Val	Leu	Val	Leu	Pro	Leu	Phe	Ile		
			215					220					225				
ttt	aca	ttt	ctc	tat	gtg	caa	atg	aga	aaa	aca	cta	agg	ttc	agg	gag	777	
Phe	Thr	Phe	Leu	Tyr	Val	Gln	Met	Arg	Lys	Thr	Leu	Arg	Phe	Arg	Glu		
		230					235					240					
cag	agg	tat	agc	ctt	ttc	aag	ctt	gtt	ttt	gcc	gta	atg	gta	gtc	ttc	825	
Gln	Arg	Tyr	Ser	Leu	Phe	Lys	Leu	Val	Phe	Ala	Val	Met	Val	Val	Phe		
	245					250					255						
ctt	ctg	atg	tgg	gcg	ccc	tac	aat	att	gca	ttt	ttc	ctg	tcc	act	ttc	873	
Leu	Leu	Met	Trp	Ala	Pro	Tyr	Asn	Ile	Ala	Phe	Phe	Leu	Ser	Thr	Phe		
260					265					270					275		
aaa	gaa	cac	ttc	tcc	ctg	agt	gac	tgc	aag	agc	agc	tac	aat	ctg	gac	921	
Lys	Glu	His	Phe	Ser	Leu	Ser	Asp	Cys	Lys	Ser	Ser	Tyr	Asn	Leu	Asp		
				280					285					290			
aaa	agt	gtt	cac	atc	act	aaa	ctc	atc	gcc	acc	acc	cac	tgc	tgc	atc	969	
Lys	Ser	Val	His	Ile	Thr	Lys	Leu	Ile	Ala	Thr	Thr	His	Cys	Cys	Ile		
			295					300					305				
aac	cct	ctc	ctg	tat	gcg	ttt	ctt	gat	ggg	aca	ttt	agc	aaa	tac	ctc	1017	



Asn Pro Leu Leu Tyr Ala Phe Leu Asp Gly Thr Phe Ser Lys Tyr Leu  
 310 315 320

tgc cgc tgt ttc cat ctg cgt agt aac acc cca ctt caa ccc agg ggg 1065  
 Cys Arg Cys Phe His Leu Arg Ser Asn Thr Pro Leu Gln Pro Arg Gly  
 325 330 335

cag tct gca caa ggc aca tcg agg gaa gaa cct gac cat tcc acc gaa 1113  
 Gln Ser Ala Gln Gly Thr Ser Arg Glu Glu Pro Asp His Ser Thr Glu  
 340 345 350 355

gtg taaactagca tccaccaaat gcaagaagaa taaacatgga ttttcatctt 1166  
 Val

tctgcattat ttcattgtaaa ttttctacac atttgtatac aaaatcggat acaggaagaa 1226  
 aagggagagg tgagctaaca tttgctaagc actgaatttg tctcaggcac cgtgcaaggc 1286  
 tctttacaaa cgtgagctcc ttgcctcct accacttgct catagtgtgg ataggactag 1346  
 tctcatttct ctgagaagaa aactaaggcg cggaaatttg tctaagatca cataactagg 1406  
 aagtggcaga actgattctc cagccctggt agcatttgct cagagcctac gcttgggtcca 1466  
 gaacatcaaaa ctccaaaccc tggggacaaa cgacatgaaa taaatgtatt ttaaaacata 1526  
 taaaaaaaaa aaaaaaaaaa a 1547

<210> 12  
 <211> 356  
 <212> PRT  
 <213> Homo sapiens

<400> 12

Met Ile Tyr Thr Arg Phe Leu Lys Gly Ser Leu Lys Met Ala Asn Tyr  
 1 5 10 15

Thr Leu Ala Pro Glu Asp Glu Tyr Asp Val Leu Ile Glu Gly Glu Leu  
 20 25 30

Glu Ser Asp Glu Ala Glu Gln Cys Asp Lys Tyr Asp Ala Gln Ala Leu  
 35 40 45

Ser Ala Gln Leu Val Pro Ser Leu Cys Ser Ala Val Phe Val Ile Gly  
 50 55 60

Val Leu Asp Asn Leu Leu Val Val Leu Ile Leu Val Lys Tyr Lys Gly  
65 70 75 80

Leu Lys Arg Val Glu Asn Ile Tyr Leu Leu Asn Leu Ala Val Ser Asn  
85 90 95

Leu Cys Phe Leu Leu Thr Leu Pro Phe Trp Ala His Ala Gly Gly Asp  
100 105 110

Pro Met Cys Lys Ile Leu Ile Gly Leu Tyr Phe Val Gly Leu Tyr Ser  
115 120 125

Glu Thr Phe Phe Asn Cys Leu Leu Thr Val Gln Arg Tyr Leu Val Phe  
130 135 140

Leu His Lys Gly Asn Phe Phe Ser Ala Arg Arg Arg Val Pro Cys Gly  
145 150 155 160

Ile Ile Thr Ser Val Leu Ala Trp Val Thr Ala Ile Leu Ala Thr Leu  
165 170 175

Pro Glu Phe Val Val Tyr Lys Pro Gln Met Glu Asp Gln Lys Tyr Lys  
180 185 190

Cys Ala Phe Ser Arg Thr Pro Phe Leu Pro Ala Asp Glu Thr Phe Trp  
195 200 205

Lys His Phe Leu Thr Leu Lys Met Asn Ile Ser Val Leu Val Leu Pro  
210 215 220

Leu Phe Ile Phe Thr Phe Leu Tyr Val Gln Met Arg Lys Thr Leu Arg  
225 230 235 240

Phe Arg Glu Gln Arg Tyr Ser Leu Phe Lys Leu Val Phe Ala Val Met  
245 250 255

Val Val Phe Leu Leu Met Trp Ala Pro Tyr Asn Ile Ala Phe Phe Leu  
260 265 270

Ser Thr Phe Lys Glu His Phe Ser Leu Ser Asp Cys Lys Ser Ser Tyr  
275 280 285

Asn Leu Asp Lys Ser Val His Ile Thr Lys Leu Ile Ala Thr Thr His  
 290 295 300

Cys Cys Ile Asn Pro Leu Leu Tyr Ala Phe Leu Asp Gly Thr Phe Ser  
 305 310 315 320

Lys Tyr Leu Cys Arg Cys Phe His Leu Arg Ser Asn Thr Pro Leu Gln  
 325 330 335

Pro Arg Gly Gln Ser Ala Gln Gly Thr Ser Arg Glu Glu Pro Asp His  
 340 345 350

Ser Thr Glu Val  
 355

<210> 13

<211> 355

<212> PRT

<213> Homo sapiens

<400> 13

Met Glu Thr Pro Asn Thr Thr Glu Asp Tyr Asp Thr Thr Thr Glu Phe  
 1 5 10 15

Asp Tyr Gly Asp Ala Thr Pro Cys Gln Lys Val Asn Glu Arg Ala Phe  
 20 25 30

Gly Ala Gln Leu Leu Pro Pro Leu Tyr Ser Leu Val Phe Val Ile Gly  
 35 40 45

Leu Val Gly Asn Ile Leu Val Val Leu Val Leu Val Gln Tyr Lys Arg  
 50 55 60

Leu Lys Asn Met Thr Ser Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp  
 65 70 75 80

Leu Leu Phe Leu Phe Thr Leu Pro Phe Trp Ile Asp Tyr Lys Leu Lys  
 85 90 95

Asp Asp Trp Val Phe Gly Asp Ala Met Cys Lys Ile Leu Ser Gly Phe  
 100 105 110

Tyr Tyr Thr Gly Leu Tyr Ser Glu Ile Phe Phe Ile Ile Leu Leu Thr  
 115 120 125

Ile Asp Arg Tyr Leu Ala Ile Val His Ala Val Phe Ala Leu Arg Ala  
 130 135 140

Arg Thr Val Thr Phe Gly Val Ile Thr Ser Ile Ile Ile Trp Ala Leu  
 145 150 155 160

Ala Ile Leu Ala Ser Met Pro Gly Leu Tyr Phe Ser Lys Thr Gln Trp  
 165 170 175

Glu Phe Thr His His Thr Cys Ser Leu His Phe Pro His Glu Ser Leu  
 180 185 190

Arg Glu Trp Lys Leu Phe Gln Ala Leu Lys Leu Asn Leu Phe Gly Leu  
 195 200 205

Val Leu Pro Leu Leu Val Met Ile Ile Cys Tyr Thr Gly Ile Ile Lys  
 210 215 220

Ile Leu Leu Arg Arg Pro Asn Glu Lys Lys Ser Lys Ala Val Arg Leu  
 225 230 235 240

Ile Phe Val Ile Met Ile Ile Phe Phe Leu Phe Trp Thr Pro Tyr Asn  
 245 250 255

Leu Thr Ile Leu Ile Ser Val Phe Gln Asp Phe Leu Phe Thr His Glu  
 260 265 270

Cys Glu Gln Ser Arg His Leu Asp Leu Ala Val Gln Val Thr Glu Val  
 275 280 285

Ile Ala Tyr Thr His Cys Cys Val Asn Pro Val Ile Tyr Ala Phe Val  
 290 295 300

Gly Glu Arg Phe Arg Lys Tyr Leu Arg Gln Leu Phe His Arg Arg Val  
 305 310 315 320

Ala Val His Leu Val Lys Trp Leu Pro Phe Leu Ser Val Asp Arg Leu  
                   325                                  330                                  335

Glu Arg Val Ser Ser Thr Ser Pro Ser Thr Gly Glu His Glu Leu Ser  
                   340                                  345                                  350

Ala Gly Phe  
           355

<210> 14

<211> 374

<212> PRT

<213> Homo sapiens

<400> 14

Met Leu Ser Thr Ser Arg Ser Arg Phe Ile Arg Asn Thr Asn Glu Ser  
   1                  5                                  10                                  15

Gly Glu Glu Val Thr Thr Phe Phe Asp Tyr Asp Tyr Gly Ala Pro Cys  
                   20                                  25                                  30

His Lys Phe Asp Val Lys Gln Ile Gly Ala Gln Leu Leu Pro Pro Leu  
           35                                  40                                  45

Tyr Ser Leu Val Phe Ile Phe Gly Phe Val Gly Asn Met Leu Val Val  
           50                                  55                                  60

Leu Ile Leu Ile Asn Cys Lys Lys Leu Lys Cys Leu Thr Asp Ile Tyr  
   65                                  70                                  75                                  80

Leu Leu Asn Leu Ala Ile Ser Asp Leu Leu Phe Leu Ile Thr Leu Pro  
                   85                                  90                                  95

Leu Trp Ala His Ser Ala Ala Asn Glu Trp Val Phe Gly Asn Ala Met  
                   100                                  105                                  110

Cys Lys Leu Phe Thr Gly Leu Tyr His Ile Gly Tyr Phe Gly Gly Ile  
           115                                  120                                  125

Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg Tyr Leu Ala Ile Val His  
 130 135 140

Ala Val Phe Ala Leu Lys Ala Arg Thr Val Thr Phe Gly Val Val Thr  
 145 150 155 160

Ser Val Ile Thr Trp Leu Val Ala Val Phe Ala Ser Val Pro Gly Ile  
 165 170 175

Ile Phe Thr Lys Cys Gln Lys Glu Asp Ser Val Tyr Val Cys Gly Pro  
 180 185 190

Tyr Phe Pro Arg Gly Trp Asn Asn Phe His Thr Ile Met Arg Asn Ile  
 195 200 205

Leu Gly Leu Val Leu Pro Leu Leu Ile Met Val Ile Cys Tyr Ser Gly  
 210 215 220

Ile Leu Lys Thr Leu Leu Arg Cys Arg Asn Glu Lys Lys Arg His Arg  
 225 230 235 240

Ala Val Arg Val Ile Phe Thr Ile Met Ile Val Tyr Phe Leu Phe Trp  
 245 250 255

Thr Pro Tyr Asn Ile Val Ile Leu Leu Asn Thr Phe Gln Glu Phe Phe  
 260 265 270

Gly Leu Ser Asn Cys Glu Ser Thr Ser Gln Leu Asp Gln Ala Thr Gln  
 275 280 285

Val Thr Glu Thr Leu Gly Met Thr His Cys Cys Ile Asn Pro Ile Ile  
 290 295 300

Tyr Ala Phe Val Gly Glu Lys Phe Arg Ser Leu Phe His Ile Ala Leu  
 305 310 315 320

Gly Cys Arg Ile Ala Pro Leu Gln Lys Pro Val Cys Gly Gly Pro Gly  
 325 330 335

Val Arg Pro Gly Lys Asn Val Lys Val Thr Thr Gln Gly Leu Leu Asp  
 340 345 350

Gly Arg Gly Lys Gly Lys Ser Ile Gly Arg Ala Pro Glu Ala Ser Leu  
 355 360 365

Gln Asp Lys Glu Gly Ala  
 370

<210> 15

<211> 355

<212> PRT

<213> Homo sapiens

<400> 15

Met Thr Thr Ser Leu Asp Thr Val Glu Thr Phe Gly Thr Thr Ser Tyr  
 1 5 10 15

Tyr Asp Asp Val Gly Leu Leu Cys Glu Lys Ala Asp Thr Arg Ala Leu  
 20 25 30

Met Ala Gln Phe Val Pro Pro Leu Tyr Ser Leu Val Phe Thr Val Gly  
 35 40 45

Leu Leu Gly Asn Val Val Val Val Met Ile Leu Ile Lys Tyr Arg Arg  
 50 55 60

Leu Arg Ile Met Thr Asn Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp  
 65 70 75 80

Leu Leu Phe Leu Val Thr Leu Pro Phe Trp Ile His Tyr Val Arg Gly  
 85 90 95

His Asn Trp Val Phe Gly His Gly Met Cys Lys Leu Leu Ser Gly Phe  
 100 105 110

Tyr His Thr Gly Leu Tyr Ser Glu Ile Phe Phe Ile Ile Leu Leu Thr  
 115 120 125

Ile Asp Arg Tyr Leu Ala Ile Val His Ala Val Phe Ala Leu Arg Ala  
 130 135 140

Arg Thr Val Thr Phe Gly Val Ile Thr Ser Ile Val Thr Trp Gly Leu  
 145 150 155 160

Ala Val Leu Ala Ala Leu Pro Glu Phe Ile Phe Tyr Glu Thr Glu Glu  
 165 170 175

Leu Phe Glu Glu Thr Leu Cys Ser Ala Leu Tyr Pro Glu Asp Thr Val  
 180 185 190

Tyr Ser Trp Arg His Phe His Thr Leu Arg Met Thr Ile Phe Cys Leu  
 195 200 205

Val Leu Pro Leu Leu Val Met Ala Ile Cys Tyr Thr Gly Ile Ile Lys  
 210 215 220

Thr Leu Leu Arg Cys Pro Ser Lys Lys Lys Tyr Lys Ala Ile Arg Leu  
 225 230 235 240

Ile Phe Val Ile Met Ala Val Phe Phe Ile Phe Trp Thr Pro Tyr Asn  
 245 250 255

Val Ala Ile Leu Leu Ser Ser Tyr Gln Ser Ile Leu Phe Gly Asn Asp  
 260 265 270

Cys Glu Arg Ser Lys His Leu Asp Leu Val Met Leu Val Thr Glu Val  
 275 280 285

Ile Ala Tyr Ser His Cys Cys Met Asn Pro Val Ile Tyr Ala Phe Val  
 290 295 300

Gly Glu Arg Phe Arg Lys Tyr Leu Arg His Phe Phe His Arg His Leu  
 305 310 315 320

Leu Met His Leu Gly Arg Tyr Ile Pro Phe Leu Pro Ser Glu Lys Leu  
 325 330 335

Glu Arg Thr Ser Ser Val Ser Pro Ser Thr Ala Glu Pro Glu Leu Ser  
 340 345 350

Ile Val Phe  
 355



<210> 16

<211> 360

<212> PRT

<213> Homo sapiens

<400> 16

Met Asn Pro Thr Asp Ile Ala Asp Thr Thr Leu Asp Glu Ser Ile Tyr  
1 5 10 15

Ser Asn Tyr Tyr Leu Tyr Glu Ser Ile Pro Lys Pro Cys Thr Lys Glu  
20 25 30

Gly Ile Lys Ala Phe Gly Glu Leu Phe Leu Pro Pro Leu Tyr Ser Leu  
35 40 45

Val Phe Val Phe Gly Leu Leu Gly Asn Ser Val Val Val Leu Val Leu  
50 55 60

Phe Lys Tyr Lys Arg Leu Arg Ser Met Thr Asp Val Tyr Leu Leu Asn  
65 70 75 80

Leu Ala Ile Ser Asp Leu Leu Phe Val Phe Ser Leu Pro Phe Trp Gly  
85 90 95

Tyr Tyr Ala Ala Asp Gln Trp Val Phe Gly Leu Gly Leu Cys Lys Met  
100 105 110

Ile Ser Trp Met Tyr Leu Val Gly Phe Tyr Ser Gly Ile Phe Phe Val  
115 120 125

Met Leu Met Ser Ile Asp Arg Tyr Leu Ala Ile Val His Ala Val Phe  
130 135 140

Ser Leu Arg Ala Arg Thr Leu Thr Tyr Gly Val Ile Thr Ser Leu Ala  
145 150 155 160

Thr Trp Ser Val Ala Val Phe Ala Ser Leu Pro Gly Phe Leu Phe Ser  
165 170 175

Thr Cys Tyr Thr Glu Arg Asn His Thr Tyr Cys Lys Thr Lys Tyr Ser  
 180 185 190

Leu Asn Ser Thr Thr Trp Lys Val Leu Ser Ser Leu Glu Ile Asn Ile  
 195 200 205

Leu Gly Leu Val Ile Pro Leu Gly Ile Met Leu Phe Cys Tyr Ser Met  
 210 215 220

Ile Ile Arg Thr Leu Gln His Cys Lys Asn Glu Lys Lys Asn Lys Ala  
 225 230 235 240

Val Lys Met Ile Phe Ala Val Val Val Leu Phe Leu Gly Phe Trp Thr  
 245 250 255

Pro Tyr Asn Ile Val Leu Phe Leu Glu Thr Leu Val Glu Leu Glu Val  
 260 265 270

Leu Gln Asp Cys Thr Phe Glu Arg Tyr Leu Asp Tyr Ala Ile Gln Ala  
 275 280 285

Thr Glu Thr Leu Ala Phe Val His Cys Cys Leu Asn Pro Ile Ile Tyr  
 290 295 300

Phe Phe Leu Gly Glu Lys Phe Arg Lys Tyr Ile Leu Gln Leu Phe Lys  
 305 310 315 320

Thr Cys Arg Gly Leu Phe Val Leu Cys Gln Tyr Cys Gly Leu Leu Gln  
 325 330 335

Ile Tyr Ser Ala Asp Thr Pro Ser Ser Ser Tyr Thr Gln Ser Thr Met  
 340 345 350

Asp His Asp Leu His Asp Ala Leu  
 355 360

<210> 17

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> HPRT sense primer

<400> 17

gtaatgatca gtcaacgggg gac

23

<210> 18

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> HPRT antisense primer

<400> 18

ccagcaagct tgcaacctta acca

24

<210> 19

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> FLAG epitope tag sequence

<400> 19

Asp Tyr Lys Asp Asp Asp Asp Lys Leu  
1 5

<210> 20

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> TECK sense primer

<400> 20

ccttcaggta tctggagagg agatc

25

<210> 21

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> TECK antisense primer

<400> 21

cacgcttgta ctgttggggt tc

22

<210> 22

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> exon 1-specific CRAM primer

<400> 22

agacgcttca gagatcctct ggaggcc

27

<210> 23

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> exon 2-specific CRAM primer

<400> 23

gaagctgctt cggggggtga gcaaac

26

<210> 24

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> exon 3-specific CRAM primer

<400> 24

caaacacagc agagcagagt gatggcacc

29

<210> 25

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> CRAM primer

<400> 25

gtgtcctggc atgggtaaca gcc

23

<210> 26

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> CRAM primer

<400> 26

cggtggaatg gtcaggttct tccc

24